Title: SOMATOSTATINS AND METHODS
Applicant(s): Mark A Sheridan et al.
Serial No.: 09/727,7
"Express Mail" Num.

EL 776900900 US Sheet 1 of 8 APPROVED O.G. FIG. 86 SS-14-I RK YG Preprosomatostatin II" DRAFTSMAN 숦 SS II" mRNA œ -24 5 The light Harmon and the light of the state of the light lig 000 8 SS-14-II RK YG Preprosomatostatin II' SS II' mRNA œ +-24 Ω I 000 83 SS-14 RK YG Preprosomatostatin I **SS-26** SS I mRNA œ

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APPROVED O.G. FIG.

BV CLASS SUBCLASS DRAFTSWAN

PPSS-I

81	
3 5'GGGGGGGGGGGAACAGGAGCAGAACTCAAAGAGAAGCCAATCTCAACGATTGTCTGCCCAATTGAACCACTTTATCC	
<u></u>	
SEQ ID NO	

	152 -88	214 -67	272 -46	340 -25	403	466	549 632 715
	CTC	CTG	GAG Glu	GGC Gly	CGT Arg	ACTC	CTCT AAAG ATTG
	CTA	CAG Gln	GTA Val	CAT His	CCA Pro	TGAATCTACTC	CCTCC
	GCA	CGC Arg	CTC	TCT Ser	GCT Ala		PAACC TTTC
	CTA	CTC Leu	ACA Thr	ATG Met	CTG	TAA ***	GACT
	GCC	AAA Lys	AAT Asn	gac Asp	GTA Val	TGT Cys	CATG
	TGC	GCC Ala	AGG Arg	GAT Asp	CCA Pro	TCG Ser	GCAC
	CAG Gln	GAT Asp	GCC Ala	$_{ m Leu}$	GGC Gly	ACA Thr	CGCT
	GTC	TCC Ser	CTT Leu	GAA Glu	CCC Pro	TTT Phe	BAATC CTAT
	CGT	CCG	GAG Glu	ATT Ile 1	GCA Ala	ACC Thr	TGCTG TGTTT TGTGZ
	ACG	GCT Ala	CAG Gln	GCG Ala	CGT Arg	AAG Lys	CCATT CTGAT CGACT
	TCG	GCC	AAA Lys	GAG Glu	GAG Glu	TGG Trp	CTTTACTGTGTGTACTACATCTCATCTCTTTTGTTTCAATCACTCATTGCTGAATCCAATGCACCATGGCCTAACCTTCTCTCTTCTAAAAAAGAAAG
	ATG CTC TCG Met Leu Ser	TCT Ser	GGC Gly	AAC Asn	CTG	TTC	CCAAT CAATC FTCTC
	ATG	GTC Val	GCA Ala	GAG Glu	GAG Glu	TTC	rgtti rtaac scggj vaaaa
	AAG 3	AGC Ser	CCT	GTA Val	CTC	AAC Asn	AACTI STATC
	CAGAAGAAG ID NO: 3	AGC Ser	GCA Ala	CAT His	GAT Asp	TGC AAG Cys Lys	TATE VAATO
	GACCCP SEQ II	ATC Ile	ATG	GCA Ala	GTG Val		CCTCA ACTGI YTACA
	GAGA	GCC	CTC	CTC	GAT Asp	GGA Gly	AAACA IGITIC
	ATCCTCTGCCTCCCCGAGACCCAGAAGAAG SEQ ID NO: 3	CTG	TCA	GAG Glu	GAG Glu	GCT Ala	STACT VAATI VGAAT
	CCTC	GCC Ala	CGG Arg	TCA	CAG Gln	AAG Lys	STGTC ATTTZ AGAAZ
	TCT	CTA	CAA Gln	CIC	GAG Glu	CGC <b>Arg</b>	racto
•	ATCC	TCC	CTC	CTA	GTG Val	GAA	CTT. TCA GAA( TTTC
)				•			

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0.G. FIG.	CLASS SUBCLASS	
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H. C. III W. II C. I. C. C. C. C. C. C. C. C.

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75. 70	139/-91 134/-87	196/-72 191/-68	253/-53 248/-49	304/-35 305/-30	358/-18 350/-14	415/+2 398/+2	477	552 535
<pre>PPSS-II' and PPSS-II" accaggcctgctccataccgactgatccagatcgagcatagcccggtccagctcgtctcaccgcgtgcca accaggcctgctccatatcaactgatctagatccagcacaccccggtccagcttagctc*****accgtgtctgg</pre>	SEQ ID NO: 9 Lys Cys Arg tccctgcaaacaaaaccaagctctgttggag ATG AGG GTC TGC CGA ATC CAC TGT GCC CTG GCC tccctgcaaacccaactcagctctgttggag ATG AGG GTC TCC CAA ATC CAC TGT GCA CTG GCC SEQ ID NO: 15 Met Arg Val Ser Gln Ile His Cys Ala Leu Ala	CTG CTG GGT TTG GCC CTG GCC ATT TGC AGC CAA GGA GCC GCC TCG CAG CCC GAC CTG CTG CTG GCT CTG GCC CTG GCA ATT TGC AGC CAA GGA GCC GCC TCG CAG CCA GAC CTG Leu Leu Gly Leu Ala Leu Ala Ile Cys Ser Gln Gly Ala Ala Ser Gln Pro Asp Leu	Arg GAC CTC CGC AGC CGC AGA CTC CTT CAG AGG GCT CGT GCC GCT GCA TTG CCA CAC AGG GAC CTC GCG AGC CGC CGA CTC CTC CAG AGG GCC CTG GCC GCT GCA TTG CCA CAC AGG ASp Leu Ala Ser Arg Arg Leu Leu Gln Arg Ala Leu Ala Ala Leu Pro His Arg	AGT GGA GTA AGC GAG CGG TGG AGG ACA TTC TAT CCC AAC TGT CCT TGC CTG *** *** AGT GGA GTA AGC GAG CGA TGG ACA TTC TAT CCG AAC TGT CCT TGC CTG AGG TGG Ser Gly Val Ser Glu Arg Trp Arg Thr Phe Tyr Pro Asn Cys Pro Cys Leu Arg Trp	AGG CCC AGG AAA GTG AAG TGT CAA *** GCG GGG GCT AAA GAG GAC CTG CGT GTG GAG AGG CCC AGA AAA GTG AAG GGT CCA CAG CTG AAG GCC AAA GAG GAC *** *** *** ATG Pro Arg Lys Val Lys Gly Pro Gln Leu Lys Ala Lys Glu Asp	CTG GAG CGC TCA GTG GGC AAC CCC AAC AAC CTT CCC CCC CGT GAG CGC AAA GCC GGC CTG GAG CGC TCA GTG GAC *** *** AAC CTT CCC CCC CGC GAG CGC AAA GCT GGC CTG GAG CGC TCA GTG GAC *** A** AAC CTT CCC CCC CGC GAG CGC AAA GCT GGC Leu Glu Arg Ser Val Asp	TGC AAG AAC TTC TAC TGG AAG GGC TTC ACT TCC TGC tga gggaagaataaaccgaccactt TGC AAG AAC TTC TAC TGG AAG GGA TTC ACT TCT TGC taa gggaagaaaagcctgaccacctt Cys Lys Asn Phe Tyr Trp Lys Gly Phe Thr Ser Cys ###	atgacatgacgctgccaatcacgtcacaccgccaacttacacctgacgaatgcagccaatcaacagttagctgtgatgacacaatgcaattcaactagctgtgatgacacacac
PPSS-II'	PPSS-II'	PPSS-II" PPSS-II"	PPSS-II'	PPSS-II'	PPSS-II'	PPSS-II'	PPSS-II'	"II-SSdd
SEQ ID NO: 14 SEQ ID NO: 20								

PPSS-II'

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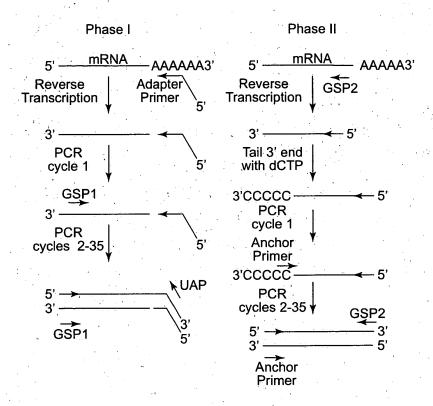


Fig. 4

Title: SOMATOSTATINS AND METHODS
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APPROVED O.G. FIG.
RV CLASS SUBCLASS B

Nulceotide Identity

54.5	52.5	72.5	8.95	72.2	78.3	84.3	82.2	95.5	2.86	H
52.8	49.8	69.4	56.8	67.7	75.5	84.3	91.2	94.4	M	100
51.1	48.0	69.4	55.3	68.4	62.6	84.3	92.4	В	98.5	98.5
51.5	49.5	6.79	53.8	2.78	74.5	84.1	뇜	0'26	36.2	2.78
52.0	0.03	6.89	55.1	2.89	0.27	<b>O</b>	6'28	9.88	6'06	91.7
51.0	20.0	2.79	8.85	2.39	ା ଧଣ	8.87	0.87	8.87	8.87	1.78
52.3	44.9	0.77	1.09	130	64.4	9.69	67.9	9:69	62.9	68.2
43.7	39.1	58.1	I ∄∀	52.3	49.2	46.2	45.5	46.2	46.2	47.7
49.0	48.2	I XIL	52.3	23.5	2.07	2.99	65.2	2.99	64.4	73.5
82.8	TR !!!"	43.9	35.6	40.9	44.7	38.6	38.6	38.6	38.6	42.4
TRI	84.1	45.5	35.6	44.7	47.7	42.4	42.4	42.4	42.4	45.5

Amino Acid Identity

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0.G. FIG.	SLASS SUBCLASS	
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Тa	
prosomatostatin	
from	
Derived	
Peptides	
of	l
Sequences	
Acid	
Amino	
of	
Comparison of Amino Acid Sequences of Peptides Derived from Pre	

comparison of America sequences of reperces beryed in	prince personal rechrosomaconer.	1 111			
	-20	-10	+1	+10 +14	
Rainbow trout <sup>b</sup>		* * PVLAPRE	KAGCKNFF	KTFTS	ID NO:
Hadfishd	AVERPROD	GQVHEPPGRE	GCKNFF	KTFTS	ID NO:
Lamprevd	. **		GCKNFF	KTFTS	ID NO:
Torpedod			GCKNFF	KTFTS	ID NO:
Ratfishd			GCKSFF	KTFTS	ID NO:
Bowfind	A S	N * * PALAPRE	GCKNFF	KTFTS	ID NO:
Sturgeond			PCKNFF	KTFTS	ID NO:
Catfishd		•	AGCKNFFW	KTFTSC	SEQ ID NO: 1
Salmond			GCKNFF	KTFTS	ID NO:
Anglerfish	AA	SGGPLLAPRE	GCKNFF	KTFTS	ID NO:
Eeld	•		GCKNFF	KTFTS	ID NO:
Flounderd			GCKNFY	KGFTS	ID NO:
Sculpind			GCKNFY	KGFTS	ID NO:
Frogê			GCKNFF	KTFTS	ID NO:
Salamanderd			GCKNFF	KTFTS	ID NO:
Alligatord			GCKNFF	KTFTS	ID NO:
Pigeond			GCKNFF	KTFTS	
Ovined	S A	NSNPAMAPRE	CKNF	KTFTS	
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CLASS SUBCLASS APPROVED O.G. FIG. DHAFTSMAN 9≺

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Sequence comparison

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		CFIIMSSSPLRLALALMCLVSAVGVISCGRP	AFII  MOCIRCPAILALLALVLCGPSVSSQLDREQSDNQDLDLELRQHWLLERARSAGLLSQEWSKRA	-	<u> </u>	MIGSAGTLILLILIAW-GARALSQ	MLSTRVOCALALLSLALAISSVSAAPS	CFIMPSTRIOCALALLAVALSVCSVSGAPSDAKLRQFLQRSILAPSVKQELTRYT	Σ			MISCRLOCALALLSIALAVGTVSAAPS		MLSCRLQCALAALSIVLALGGVTGAPSDPRLRQFLQKSLAAAAGKQELAKYF	MISCRLQCALAALSIVLALGCVTGAPSDPRLRQFLQKSLAAAAGKQELAKYF	MLSCRLQCALAALSIVLALGCVTGAPSDPRLRQFLQKSLAAAGKQELAKYF
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_	15	36	37	. 8	9 6	40		4	4.7	4 کے	44	4.5	46	47	48	49

continued)

LABILLS-EPNOTENDALEPEDLSOAAE-QDEMRLELORSANS-NPAMAPRERKAGCKNFFWKTFTSC LAELLS-EPNQTENDALEPEDLPQAAE-QDEMRLELQRSANS-NPAMAPRERKAGCKNFFWKTFTSC LAELLS-EPNOTENDALEPEDLSQAAE-QDEMRLELQRSANS-NPAMAPRERKAGCKNFFWKTFTSC WRTFYPNCPCLRWRPRKVKGPQLKAKE-DL-----ERSV----DNLPPRERKAGCKNFYWKGFTSC LPELQW-MLSNNELTPVQVEEAPRS-----RLELVRRDN----T-VTSKPINCMNYFWKSRTAC VEELLAQMSLPEATFQREAEDASMATE-G---RMNLERSVDS-TNNLPPRERKAGCKNFYWKGFTSC VEKLLSLLSIPEMEMR--EKGLSMAGE-SEDLRLEQERSAES-SNQLPTRVRKEGCKNFYWKGFTSC LVELLS-ELAHVENEAIELDDMSHGVE-QEDVDLELERAPG---PVLAPRERKAGCKNFFWKTFTSC LAELLLSDLLQGENEALEEENFPLAEGGPEDAHADLERAASG-GPLLAPRERKAGCKNFFWKTFTSC WRTFYPNCPCLR--PRKVKCP-AGAKE-DLR--VELERSVGN-PNNLPPRERKAGCKNFYWKGFTSC SGLLD--GVDNSVLDGEIAPVPFDAEEPLESRLE-ERAVYNRLSQLPQRDRKAPCKNFFWKTFTSC LSGWTD--S-RESNLVEVERNVPDPPE-P----KIPPSVK--FPRLSLRERKAPCKNFFWKTFTMC LAELLA-ELAEAENEVLDSDEVSRAAE-SEGARLEMERAAG---PMLAPRERKAGCKNFFWKTFTSC LADLLS-ELVQAENEALEPEDLSRAVE-KDEVRLELERAAG---PMLAPRERKAGCKNFFWKTFTS( LAELLS-EPSQTENEALESEDLSRGAE-QDEVRLELERSANS-NPALAPRERKAGCKNFFWKTFTS( Laells-epnoteidalepedlsqaae-qdemrlelqrsans-npamaprerkagcknffwktfts( LAELLS-EPSQTDNEALESDDLPRGAE-QDEVRLELERSANS-SPALAPRERKAGCKNFFWKTFTS

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Applicant(s): Mar Sheridan et al.
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APPROVED O.G. FIG.

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